

Fig. 1

PPSS-I

SEQ ID NO: 8 5'GGGGGGGGGAACAGGAGCAGCAGAACTCAAGAGAGCAATCTCAACGATTGTCTGCCCAATTGAACCACTTTATCC 81

ATCCTCTGCCCTCCCCGAGACCCAGAGAAG ATG CTC TCG ACG CGT GTC CAG TGC GCC CTA GCA CTA CTC 152
SEQ ID NO: 3 Met Leu Ser Thr Arg Val Gln Cys Ala Leu Ala Leu Leu -88

TCC CTA GCC CTG GCC ATC AGC AGC GTC TCT GCC GCT CCG TCC GAT GCC AAA CTC CGC CAG CTG 214
Ser Leu Ala Leu Ala Ile Ser Ser Val Ser Ala Ala Pro Ser Asp Ala Lys Leu Arg Gln Leu -67

CTC CAA CGG TCA CTC ATG GCA CCT GCA GGC AAA CAG GAG CTT GCC AGG AAT ACA CTC GTA GAG 272
Leu Gln Arg Ser Leu Met Ala Pro Ala Gly Lys Gln Glu Leu Ala Arg Asn Thr Leu Val Glu -46

CTA CTC TCA GAG CTC GCA CAT GTA GAG AAC GAG GCG ATT GAA TTG GAT GAC ATG TCT CAT GGC 340
Leu Leu Ser Glu Leu Ala His Val Glu Asn Glu Ala Ile Glu Leu Asp Asp Met Ser His Gly -25

GTG GAG CAG GAG GAT GTG GAT CTC GAG CTG GAG CGT GCA CCC GGC CCA GTA CTG GCT CCA CGT 403
Val Glu Gln Glu Asp Val Asp Leu Glu Leu Glu Arg Ala Pro Gly Pro Val Leu Ala Pro Arg -4

GAA CGC AAG GCT GGA TGC AAG AAC TTC TTC TGG AAG ACC TTT ACA TCG TGT TAA TGAATCTACTC 466
Glu Arg Lys Ala Gly Cys Lys Asn Phe Phe Trp Lys Thr Phe Thr Ser Cys ***

CTTTACTGTGTACTACATCTCATCTCTTTTGTTCATCACTCATCTGCTGAATCCAATGCACCATGGCCTAACCCCTCTCT 549
TCAAAAAATTAAATAAACACTGTTATAACTTTAACAATCATCTGATGTTTCTATCGCTCACTTAGATTTTTCGAAAAAG 632
GAACACAAGAAAGAAATGTTCTACAAATGTATGCGGTTCTGCTTTGACTGTGATTTATGTATTTTGGCAGACTATTTTAAATTG 715
TTTGTGTAATAAAATCTGTGTTTCAGAACCAAAAAAATAAAAAA 3'

Fig. 2

PPSS-II' and PPSS-II"		
SEQ ID NO: 14 PPSS-II'	accaggcctgctccataccgactgacccagatccagatcgagcatagcccggtccagctcagctcgtcaccgcgtgccca	75
SEQ ID NO: 20 PPSS-II"	accaggcctgctccataccgactgacccagatccagatcgagcatagcccggtccagctcagctcgtcaccgcgtgccca	70
SEQ ID NO: 9 Lys Cys Arg		
PPSS-II'	tccctgcaaaaaccagctctgttgag ATG AAG GTC TGC CGA ATC CAC TGT GCC CTG GCC	139/-91
PPSS-II"	tccctgcaaaaaccagctctgttgag ATG AAG GTC TGC CAA ATC CAC TGT GCA CTG GCC	134/-87
SEQ ID NO: 15 Met Arg Val Ser Gln Ile His Cys Ala Leu Ala		
PPSS-II'	CTG CTG GGT TTG GCC CTG GCC ATT TGC AGC CAA GGA GCC TCG CAG CCC GAC CTG	196/-72
PPSS-II"	CTG CTG GGT TTG GCC CTG GCA ATT TGC AGC CAA GGA GCC TCG CAG CCA GAC CTG	191/-68
Leu Leu Gly Leu Ala Leu Ala Ile Cys Ser Gln Gly Ala Ala Ser Gln Pro Asp Leu		
Arg		
PPSS-II'	GAC CTC CGC AGC CGC AGA CTC CTT CAG AGG GCT CGT GCC GCT GCA TTG CCA CAC AGG	253/-53
PPSS-II"	GAC CTC GCG AGC CGC CGA CTC CTC CAG AGG GCT CGT GCC GCT GCA TTG CCA CAC AGG	248/-49
Asp Leu Ala Ser Arg Arg Leu Leu Gln Arg Ala Leu Ala Leu Pro His Arg		
PPSS-II'	AGT GGA GTA AGC GAG CGG TGG AGG ACA TTC TAT CCC AAC TGT CCT TGC CTG ***	304/-35
PPSS-II"	AGT GGA GTA AGC GAG CGA TGG AGG ACA TTC TAT CCC AAC TGT CCT TGC CTG AGG TGG	305/-30
Ser Gly Val Ser Glu Arg Trp Arg Thr Phe Tyr Pro Asn Cys Pro Cys Leu Arg Trp		
Cys		
PPSS-II'	AGG CCC AGG AAA GTG AAG TGT CAA *** GCG GGG GCT AAA GAG GAC CTG CGT GTG GAG	358/-18
PPSS-II"	AGG CCC AGA AAA GTG AAG GGT CCA CAG CTG AAG GCC AAA GAG GAC *** ***	350/-14
Arg Pro Arg Lys Val Lys Gly Pro Gln Leu Lys Ala Lys Glu Asp		
Leu Arg Val Glu		
PPSS-II'	CTG GAG CGC TCA GTG GGC AAC CCC AAC AAC CTT CCC CCC CGT GAG CGC AAA GCC GGC	415/+2
PPSS-II"	CTG GAG CGC TCA GTG GGC *** *** AAC CTT CCC CCC CGC GAG CGC AAA GCT GGC	398/+2
Leu Glu Arg Ser Val Asp		
Asn Leu Pro Pro Arg Glu Arg Lys Ala Gly		
PPSS-II'	TGC AAG AAC TTC TAC TGG AAG GGC TTC ACT TCC TGC tga gggagaataaaaccgaccctt	477
PPSS-II"	TGC AAG AAC TTC TAC TGG AAG GGA TTC ACT TCT TGC taa gggagaataaaaccgaccctt	460
Cys Lys Asn Phe Tyr Trp Lys Gly Phe Thr Ser Cys ##		
PPSS-II'	atgacatgacgtgccaatcacgtcacacccgccaacttacacctgacgaatgcagccaatcaacagttagctgtg	552
PPSS-II"	atgacacaatgcattcaatcacatcacacccgccaacttacacctgactaatgtagccaatcagcaattagctgtg	535
PPSS-II'	cccgatgatggttcttgaaatcaacagaatgatgtacctgtctaatttgtgaaatgaaatataaaataattg(a)n	
PPSS-II"	cctgatgacaattatgattatgatgtacctgactaatttagaaaataaaagagaaaataaaagagaaac(a)n	

Fig. 3

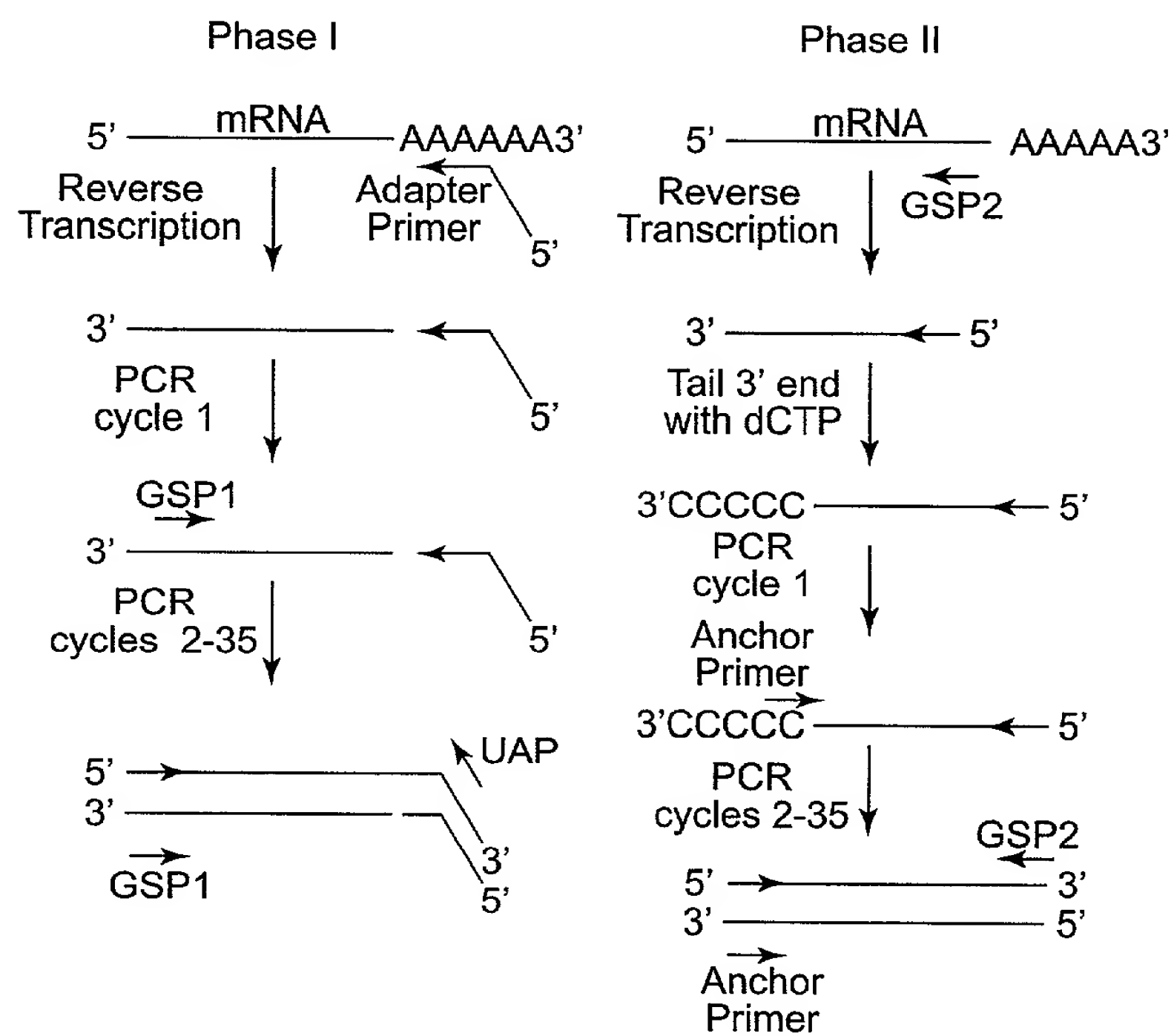


Fig. 4

Nucleotide Identity											
TRII	82.8	49.0	43.7	52.3	51.0	52.0	51.5	51.1	52.8	54.5	
84.1	TRII	48.2	39.1	44.9	50.0	50.0	49.5	48.0	49.8	52.5	
45.5	43.9	TRII	58.1	77.0	67.7	68.9	67.9	69.4	69.4	72.5	
35.6	35.6	52.3	AFI	60.1	58.8	55.1	53.8	55.3	56.8	56.8	
44.7	40.9	73.5	52.3	GFI	65.7	68.7	67.7	68.4	67.7	72.2	
47.7	44.7	70.5	49.2	64.4	FRI	75.0	74.5	62.6	75.5	78.3	
42.4	38.6	66.7	46.2	63.6	78.8	C	84.1	84.3	84.3	84.3	
42.4	38.6	65.2	45.5	62.9	78.0	87.9	R	92.4	91.2	92.2	
42.4	38.6	66.7	46.2	63.6	78.8	88.6	97.0	B	94.4	95.5	
42.4	38.6	64.4	46.2	62.9	78.8	90.9	96.2	98.5	M	98.7	
45.5	42.4	73.5	47.7	68.2	87.1	91.7	97.7	98.5	100	H	
Amino Acid Identity											

Fig. 5

Comparison of Amino Acid Sequences of Peptides Derived from Preprosomatostatin Ia

	-20	-10	+1	+10	+14	
Rainbow trout ^b						
Hagfish ^d						SEQ ID NO: 4
Lamprey ^d						SEQ ID NO: 27
Torpedo ^d						SEQ ID NO: 1
Ratfish ^d						SEQ ID NO: 1
Bowfin ^d						SEQ ID NO: 28
Sturgeon ^d						SEQ ID NO: 29
Catfish ^d						SEQ ID NO: 30
Salmon ^d						SEQ ID NO: 1
Anglerfish ^c						SEQ ID NO: 1
Eel ^d						SEQ ID NO: 31
Flounder ^d						SEQ ID NO: 1
Sculpin ^d						SEQ ID NO: 2
Frog ^c						SEQ ID NO: 2
Salamander ^d						SEQ ID NO: 1
Alligator ^d						SEQ ID NO: 1
Pigeon ^d						SEQ ID NO: 1
Ovine ^d						SEQ ID NO: 1
						SEQ ID NO: 32

Fig. 6

Sequence comparison

SEQ ID NO: 9	TRII'	---MKVCRHICALALIGLALAICSQGAASQP-----DLDLRSRLLQARAAAWPHRSGVSR	WRTFYPCPLR--PRKVKCP-AGAKE-DLR--VELERSVGN-PNNLPPRERKAGCKNFYWKGFTSC
SEQ ID NO: 15	TRII"	---MRVSIHICALALIGLALAICSQGAASQP-----DLDLASRLLQALAAALPHRSGVSR	WRTFYPCPLRWRPRKVKGPQLKAKE-DL-----ERSV-----DNLPPRERKAGCKNFYWKGFTSC
SEQ ID NO: 36	CFII	---MSSPLRLALMCLVSAVVISCCRP-----HVVINSALEEARNVPFGEEVPERLT	LPELQW-MLSNNELTPVQVEEAPRS-----RLELVRRDN-----T-VTSKPLNCMNYFWKKSRTAC
SEQ ID NO: 37	AFII	---MQCIRCPAILALLALVLCGPSVSSQLDREQSDNQDLDLELRQHLLERARSAGLLSQEWSKRA	VEELLAQMSLPEATFQREAEADASMATE-G-----RMNLEERSVDS-TNNLPPRERKAGCKNFYWKGFTSC
SEQ ID NO: 38	GFII	---MRLCELHCYLALLGLSLVLCGRCAANSQ--EP-----DLDLFRHRLQASATQATQDFTKRD	VEKLILLSIPEMEMR--EKGLSMAGE-SEDLRLQEERSAES-SNQLPTRVRKEGCKNFYWKGFTSC
SEQ ID NO: 39	GFIII	---MQLSSIVSLLLVLSVRAAAVL-----PVEERNPAQSRELSKE-RKELILKL	ISGLLD--GVDNSVLDGEIAPVPFDAAEEPLESRLE-ERAVYNRLSQLPQDRKAPCKNFFWKTFITMC
SEQ ID NO: 40	FRII	---MLGSAGTLLLLLAW-GARALSQ-----PDDNRITTTGRNQDLNAIQQDLLLLKL	LSGWTD--S-RESNLVEVERNVPDPPE-P-----KIPPSVK--FPRLSLRERKAPCKNFFWKTFITMC
SEQ ID NO: 3	TRI	---MLSTRVQCALALLSLAIAISSVSAAPS-----DAKLRLQFLQRSILAPSVKQELTRYT	LVELLS-ELAHVENEAEIELDDMSHGVE-QEDVDLELERAPG--PVLAPRERKAGCKNFYWKTFITSC
SEQ ID NO: 41	CFI	---MPSTRIQCALALLAVALSVCSVSGAPS-----DAKLRLLLHRYPLQGS-KQDMTRSA	LAELLA-ELAEAEENEVLDSDEVSRAAE-SEGARLEMERAAAG--PMLAPRERKAGCKNFYWKTFITSC
SEQ ID NO: 42	AFI	MKMVSSSRRLRCLLVLLSLTASISCSFAGQR-----DSKLRLLLHRYPLQGS-KQDMTRSA	LAELLLDQLQGENEAELEENFPLAEGGPEDAHADLERAAAG-GPLILAPRERKAGCKNFYWKTFITSC
SEQ ID NO: 43	GFI	---MLSTRIQCALALLSLAIAVCSVSAAPT-----DAKLRLQFLQRSILNPAGKQELARYT	LADLLS-ELVQAENEAELEPEDLSRGAE-QDEVRLLEERSANS-SPALAPRERKAGCKNFYWKTFITSC
SEQ ID NO: 44	FRI	---MQSCRVCALTLTLLSIALAINSISAAPT-----DPRLRQFLQKSLASAG-KQELAKYF	LAELLS-EPSTQDNEAELEPEDLSRGAE-QDEVRLLEERSANS-SPALAPRERKAGCKNFYWKTFITSC
SEQ ID NO: 45	C	---MLSCRLQCALALLSIALAVGTVSAAPS-----DPRLRQFLQKSLAAAGKQELAKYF	LAELLS-EPNQTENDALEPEDLPQAAE-QDEMRLLEQRSANS-NPALAPRERKAGCKNFYWKTFITSC
SEQ ID NO: 46	R	---MLSCRLQCALAALCIVLALGGVTGAPS-----DPRLRQFLQKSLAAAGKQELAKYF	LAELLS-EPNQTENDALEPEDLSQAAE-QDEMRLLEQRSANS-NPALAPRERKAGCKNFYWKTFITSC
SEQ ID NO: 47	B	---MLSCRLQCALAALSIVLALGGVTGAPS-----DPRLRQFLQKSLAAAGKQELAKYF	LAELLS-EPNQTENDALEPEDLSQAAE-QDEMRLLEQRSANS-NPALAPRERKAGCKNFYWKTFITSC
SEQ ID NO: 48	M	---MLSCRLQCALAALSIVLALGCVTGAPS-----DPRLRQFLQKSLAAAGKQELAKYF	LAELLS-EPNQTENDALEPEDLSQAAE-QDEMRLLEQRSANS-NPALAPRERKAGCKNFYWKTFITSC
SEQ ID NO: 49	H	---MLSCRLQCALAALSIVLALGCVTGAPS-----DPRLRQFLQKSLAAAGKQELAKYF	LAELLS-EPNQTENDALEPEDLSQAAE-QDEMRLLEQRSANS-NPALAPRERKAGCKNFYWKTFITSC

(continued)

Fig. 7

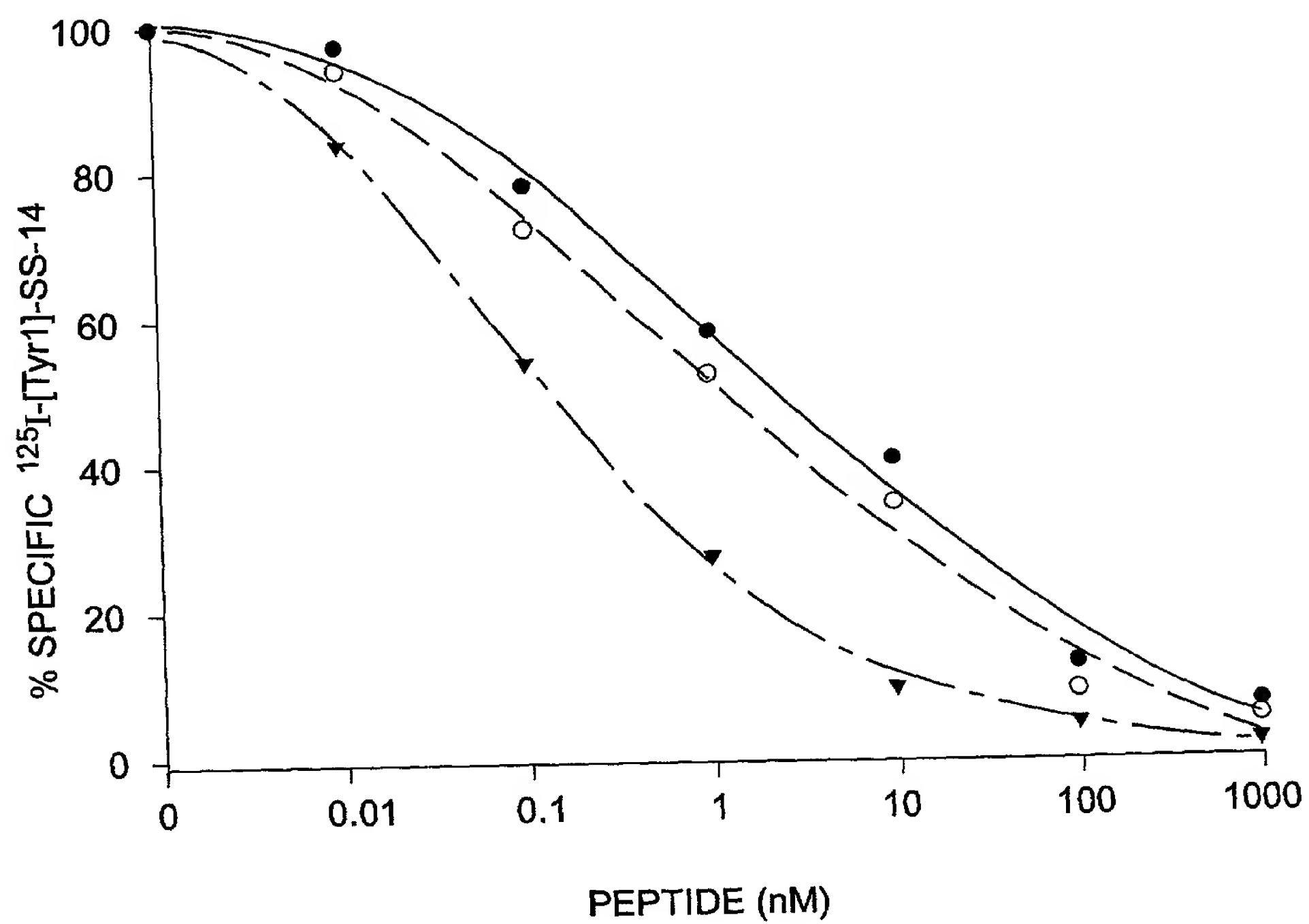


Fig. 8